

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/851,673

DATE: 05/21/2001
TIME: 09:59:12

Input Set : A:\3198 Seq Listing 050801.txt
Output Set: N:\CRF3\05212001\I851673.raw

ENTERED

3 <110> APPLICANT: Derry, Jonathan
 4 Fanslow, William
 5 Dougall, William
 7 <120> TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS OR ANTAGONISTS OF CD40 SIGNALING
 9 <130> FILE REFERENCE: 3198
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/851,673
 12 <141> CURRENT FILING DATE: 2001-05-08
 14 <160> NUMBER OF SEQ ID NOS: 4
 16 <170> SOFTWARE: PatentIn version 3.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 1994
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Homo sapiens
 23 <220> FEATURE:
 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (149)..(1405)
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 30 ccgcagacta tcaatccccag tctctccccc tcactccctg tgaagcttc cagcatcatc 120
 32 gaggtccccat cagcccttgc cctgttgg atg aat agg cac ctc tgg aag agc 172
 33 Met Asn Arg His Leu Trp Lys Ser
 34 1 5
 36 caa ctg tgt gag atg gtg cag ccc agt ggt ggc ccg gca gca gat cag 220
 37 Gln Leu Cys Glu Met Val Gln Pro Ser Gly Gly Pro Ala Ala Asp Gln
 38 10 15 20
 40 gac gta ctg ggc gaa gag tct cct ctg ggg aag cca gcc atg ctg cac 268
 41 Asp Val Leu Gly Glu Ser Pro Leu Gly Lys Pro Ala Met Leu His
 42 25 30 35 40
 44 ctg cct tca gaa cag ggc gct cct gag acc ctc cag cgc tgc ctg gag 316
 45 Leu Pro Ser Glu Gln Gly Ala Pro Glu Thr Leu Gln Arg Cys Leu Glu
 46 45 50 55
 48 gag aat caa gag ctc cga gat gcc atc cgg cag agc aac cag att ctg 364
 49 Glu Asn Gln Glu Leu Arg Asp Ala Ile Arg Gln Ser Asn Gln Ile Leu
 50 60 65 70
 52 cgg gag cgc tgc gag gag ctt ctg cat ttc caa gcc agc cag agg gag 412
 53 Arg Glu Arg Cys Glu Glu Leu Leu His Phe Gln Ala Ser Gln Arg Glu
 54 75 80 85
 56 gag aag gag ttc ctc atg tgc aag ttc cag gag gcc agg aaa ctg gtg 460
 57 Glu Lys Glu Phe Leu Met Cys Lys Phe Gln Glu Ala Arg Lys Leu Val
 58 90 95 100
 60 gag aga ctc ggc ctg gag aag ctc gat ctg aag agg cag aag gag cag 508
 61 Glu Arg Leu Gly Leu Glu Lys Leu Asp Leu Lys Arg Gln Lys Glu Gln
 62 105 110 115 120
 64 gct ctg cgg gag gtg gag cac ctg aag aga tgc cag cag cag atg gct 556
 65 Ala Leu Arg Glu Val Glu His Leu Lys Arg Cys Gln Gln Gln Met Ala
 66 125 130 135
 68 gag gac aag gcc tct gtg aaa gcc cag gtg acg tcc ttg ctc ggg gag 604

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69	Glu	Asp	Lys	Ala	Ser	Val	Lys	Ala	Gln	Val	Thr	Ser	Leu	Leu	Gly	Glu		
70				140				145								150		
72	ctg	cag	gag	agc	cag	agt	cgc	ttg	gag	gct	gcc	act	aag	gaa	tgc	cag	652	
73	Leu	Gln	Glu	Ser	Gln	Ser	Arg	Leu	Glu	Ala	Ala	Thr	Lys	Glu	Cys	Gln		
74				155				160								165		
76	gct	ctg	gag	ggt	cg	g	cc	gg	g	cc	ag	g	c	gg	ca	g	700	
77	Ala	Leu	Glu	Gly	Arg	Ala	Arg	Ala	Ala	Ser	Glu	Gln	Ala	Arg	Gln	Leu		
78				170				175								180		
80	gag	agt	gag	cgc	gag	g	cg	g	ca	g	ac	gt	g	ca	gt	g	748	
81	Glu	Ser	Glu	Arg	Glu	Ala	Leu	Gln	Gln	His	Ser	Val	Gln	Val	Asp			
82	185				190				195							200		
84	cag	ctg	cgc	atg	cag	gg	cc	ag	gt	g	cc	g	cc	tc	cg	at	g	796
85	Gln	Leu	Arg	Met	Gln	Gly	Gln	Ser	Val	Glu	Ala	Ala	Leu	Arg	Met	Glu		
86				205				210								215		
88	cgc	cag	gcc	tcg	gag	g	ag	a	ag	ctg	g	cc	ca	tg	ca	g	844	
89	Arg	Gln	Ala	Ala	Ser	Glu	Glu	Lys	Arg	Lys	Leu	Ala	Gln	Leu	Gln	Val		
90				220				225								230		
92	gcc	tat	cac	cag	ctc	ttc	caa	gaa	tac	gac	aac	ca	tc	a	ag	g	892	
93	Ala	Tyr	His	Gln	Leu	Phe	Gln	Glu	Tyr	Asp	Asn	His	Ile	Lys	Ser	Ser		
94				235				240								245		
96	gt	gt	gg	ag	g	ag	cg	g	ga	at	g	ca	tg	g	aa	g	940	
97	Val	Val	Gly	Ser	Glu	Arg	Lys	Arg	Gly	Met	Gln	Leu	Glu	Asp	Leu	Lys		
98				250				255								260		
100	cag	cag	ctc	cag	cag	gg	cc	tg	gt	gg	cc	aa	ca	g	g	gt	988	
101	Gln	Gln	Leu	Gln	Gln	Ala	Glu	Glu	Ala	Leu	Val	Ala	Lys	Gln	Glu	Val		
102	265				270				275							280		
104	atc	gat	aag	ctg	aag	gag	gg	cc	ga	ca	cc	aag	at	gt	at	g	1036	
105	Ile	Asp	Lys	Leu	Lys	Glu	Glu	Ala	Glu	Gln	His	Lys	Ile	Val	Met	Glu		
106				285				290								295		
108	acc	gtt	ccg	gt	ctg	aag	gg	cc	ca	gg	at	tc	ta	ca	gg	cc	1084	
109	Thr	Val	Pro	Val	Leu	Lys	Ala	Gln	Ala	Asp	Ile	Tyr	Lys	Ala	Asp	Phe		
110				300				305								310		
112	cag	gct	gag	agg	cag	gg	cc	tg	gg	cc	ga	aa	ag	g	gg	ct	1132	
113	Gln	Ala	Glu	Arg	Gln	Ala	Arg	Glu	Lys	Leu	Ala	Glu	Lys	Lys	Glu	Leu		
114				315				320								325		
116	ctg	cag	cag	ctg	gag	ca	tg	ca	gg	ga	tg	ac	aa	ct	g	a	1180	
117	Leu	Gln	Glu	Leu	Glu	Gln	Leu	Gln	Arg	Glu	Tyr	Ser	Lys	Leu	Lys			
118				330				335								340		
120	gcc	agc	tgt	cag	gag	tc	gg	cc	ag	at	g	gg	aa	cg	g	ca	1228	
121	Ala	Ser	Cys	Gln	Glu	Ser	Ala	Arg	Ile	Glu	Asp	Met	Arg	Lys	Arg	His		
122	345				350				355							360		
124	gtc	gag	gtc	tcc	cag	gg	cc	tt	gg	cc	cc	cct	gg	cc	tc	tc	1276	
125	Val	Glu	Val	Ser	Gln	Ala	Pro	Leu	Pro	Pro	Ala	Pro	Ala	Tyr	Leu	Ser		
126				365				370								375		
128	tct	ccc	ctg	gg	cc	agc	ca	gg	gg	agc	cc	cc	gg	gg	cc	aa	1324	
129	Ser	Pro	Leu	Ala	Leu	Pro	Ser	Gln	Arg	Arg	Ser	Pro	Pro	Glu	Glu	Pro		
130				380				385								390		
132	cct	gac	tcc	tgc	tgc	tgc	tgc	tat	cag	gg	cct	gat	at	g	ac		1372	
133	Pro	Asp	Phe	Cys	Cys	Pro	Lys	Cys	Gln	Tyr	Gln	Ala	Pro	Asp	Met	Asp		

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134	395	400	405			
136	acc ctg cag ata cat gtc atg gag tgc att gag	tagggccggc	cagtgcagg	1425		
137	Thr Leu Gln Ile His Val Met Glu Cys Ile Glu					
138	410	415				
140	ccactgcctg cccgaggacg tgcccgaa	cgtgcagtct	gegccttcct	ctccccgcctg	1485	
142	cctagcccag gatgaaggc tgggtggca	caactggat	gccacctgga	gccccaccca	1545	
144	ggagctggcc gcggcacctt acgcttcagc	tgttgatccg	ctggccctt	cttttgggt	1605	
146	agatgcggcc ccgatcagggc	ctgactcgct	gtctttttt	ttcccttctg	tctgctcgaa	1665
148	ccacttgccct cgggctaatac	cctccctt	cetccacccg	gcactgggaa	agtcaagaat	1725
150	ggggcctggg gctctcaggg agaactcgctt	cccctggca	agctgggtgg	cagctttcc	1785	
152	tcccacccga caccgacccg	cccggcgtg	tgccttgggaa	gtgctgcctt	cttaccatgc	1845
154	acacgggtgc ttccttttgc	ggctgcatgc	tattccattt	tgcagccaga	ccgatgtgt	1905
156	ttaaccagt cactattgtt	ggacatttgg	gttggggcc	atcttttgt	taccataaat	1965
158	aatggcatag taaaaaaaaaaaaaaa					1994
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162	<211> LENGTH: 419					
163	<212> TYPE: PRT					
164	<213> ORGANISM: Homo sapiens					
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168	Met Asn Arg His Leu Trp Lys Ser Gln Leu Cys Glu Met Val Gln Pro					
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172	Ser Gly Gly Pro Ala Ala Asp Gln Asp Val Leu Gly Glu Ser Pro					
173	20 25 30					
176	Leu Gly Lys Pro Ala Met Leu His Leu Pro Ser Glu Gln Gly Ala Pro					
177	35 40 45					
180	Glu Thr Leu Gln Arg Cys Leu Glu Glu Asn Gln Glu Leu Arg Asp Ala					
181	50 55 60					
184	Ile Arg Gln Ser Asn Gln Ile Leu Arg Glu Arg Cys Glu Glu Leu Leu					
185	65 70 75 80					
188	His Phe Gln Ala Ser Gln Arg Glu Glu Lys Glu Phe Leu Met Cys Lys					
189	85 90 95					
192	Phe Gln Glu Ala Arg Lys Leu Val Glu Arg Leu Gly Leu Glu Lys Leu					
193	100 105 110					
196	Asp Leu Lys Arg Gln Lys Glu Gln Ala Leu Arg Glu Val Glu His Leu					
197	115 120 125					
200	Lys Arg Cys Gln Gln Gln Met Ala Glu Asp Lys Ala Ser Val Lys Ala					
201	130 135 140					
204	Gln Val Thr Ser Leu Leu Gly Glu Leu Gln Glu Ser Gln Ser Arg Leu					
205	145 150 155 160					
208	Glu Ala Ala Thr Lys Glu Cys Gln Ala Leu Glu Gly Arg Ala Arg Ala					
209	165 170 175					
212	Ala Ser Glu Gln Ala Arg Gln Leu Glu Ser Glu Arg Glu Ala Leu Gln					
213	180 185 190					
216	Gln Gln His Ser Val Gln Val Asp Gln Leu Arg Met Gln Gly Gln Sér					
217	195 200 205					
220	Val Glu Ala Ala Leu Arg Met Glu Arg Gln Ala Ala Ser Glu Glu Lys					
221	210 215 220					
224	Arg Lys Leu Ala Gln Leu Gln Val Ala Tyr His Gln Leu Phe Gln Glu					
225	225 230 235 240					

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228 Tyr Asp Asn His Ile Lys Ser Ser Val Val Gly Ser Glu Arg Lys Arg
 229 245 250 255
 232 Gly Met Gln Leu Glu Asp Leu Lys Gln Gln Leu Gln Gln Ala Glu Glu
 233 260 265 270
 236 Ala Leu Val Ala Lys Gln Glu Val Ile Asp Lys Leu Lys Glu Glu Ala
 237 275 280 285
 240 Glu Gln His Lys Ile Val Met Glu Thr Val Pro Val Leu Lys Ala Gln
 241 290 295 300
 244 Ala Asp Ile Tyr Lys Ala Asp Phe Gln Ala Glu Arg Gln Ala Arg Glu
 245 305 310 315 320
 248 Lys Leu Ala Glu Lys Lys Glu Leu Leu Gln Glu Gln Leu Glu Gln Leu
 249 325 330 335
 252 Gln Arg Glu Tyr Ser Lys Leu Lys Ala Ser Cys Gln Glu Ser Ala Arg
 253 340 345 350
 256 Ile Glu Asp Met Arg Lys Arg His Val Glu Val Ser Gln Ala Pro Leu
 257 355 360 365
 260 Pro Pro Ala Pro Ala Tyr Leu Ser Ser Pro Leu Ala Leu Pro Ser Gln
 261 370 375 380
 264 Arg Arg Ser Pro Pro Glu Glu Pro Pro Asp Phe Cys Cys Pro Lys Cys
 265 385 390 395 400
 268 Gln Tyr Gln Ala Pro Asp Met Asp Thr Leu Gln Ile His Val Met Glu
 269 405 410 415
 272 Cys Ile Glu
 276 <210> SEQ ID NO: 3
 277 <211> LENGTH: 5371
 278 <212> TYPE: DNA
 279 <213> ORGANISM: Homo sapiens
 281 <220> FEATURE:
 282 <221> NAME/KEY: CDS
 283 <222> LOCATION: (392)..(3262)
 285 <400> SEQUENCE: 3
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 288 ttcttagggtg aggatgggtc tacacagcca cccggagttc cttagttgaa aggtgcgccc 120
 290 tgctgtgaca gaatgtggta attgtaatct ttaacatttt catgtaaaac atatttcctg 180
 292 atcatcttcc cattgtcttc atggaaaatt gataaaatatt tgtgccttcc aactctcgtc 240
 294 ttgttgaat gacttcatct taataacaaca tggacaccac gttgctgaaa acatgcttg 300
 296 ggactgccac tgaatttatac ttttgcgggtt ttatgacaaa gttatttagta gtttcccttt 360
 298 ttgaaattag tattttgaag ttaatatcac a atg agt tca ggc tta tgg agc 412
 299 Met Ser Ser Gly Leu Trp Ser
 300 1 5
 302 caa gaa aaa gtc act tca ccc tac tgg gaa gag cggtt att ttt tac ttg 460
 303 Gln Glu Lys Val Thr Ser Pro Tyr Trp Glu Glu Arg Ile Phe Tyr Leu
 304 10 15 20
 306 ctt ctt caa gaa tgc agc gtt aca gac aaa caa aca caa aag ctc ctt 508
 307 Leu Leu Gln Glu Cys Ser Val Thr Asp Lys Gln Thr Gln Lys Leu Leu
 308 25 30 35
 310 aaa gta ccg aag gga agt ata gga cag tat att caa gat cgt tct gtg 556
 311 Lys Val Pro Lys Gly Ser Ile Gly Gln Tyr Ile Gln Asp Arg Ser Val
 312 40 45 50 55

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314 ggg cat tca agg att cct tct gca aaa ggc aag aaa aat cag att gga	604
315 Gly His Ser Arg Ile Pro Ser Ala Lys Gly Lys Lys Asn Gln Ile Gly	
316 60 65 70	
318 tta aaa att cta gag caa cct cat gca gtt ctc ttt gtt gat gaa aag	652
319 Leu Lys Ile Leu Glu Gln Pro His Ala Val Leu Phe Val Asp Glu Lys	
320 75 80 85	
322 gat gtt gta gag ata aat gaa aag ttc aca gag tta ctt ttg gca att	700
323 Asp Val Val Glu Ile Asn Glu Lys Phe Thr Glu Leu Leu Leu Ala Ile	
324 90 95 100	
326 acc aat tgt gag gag agg ttc agc ctg ttt aaa aac aca aac aca cta	748
327 Thr Asn Cys Glu Glu Arg Phe Ser Leu Phe Lys Asn Arg Asn Arg Leu	
328 105 110 115	
330 agt aaa ggc ctc caa ata gac gtg ggc tgt cct gtg aaa gta cag ctg	796
331 Ser Lys Gly Leu Gln Ile Asp Val Gly Cys Pro Val Lys Val Gln Leu	
332 120 125 130 135	
334 aga tct ggg gaa gaa aaa ttt cct gga gtt gta cgc ttc aga gga ccc	844
335 Arg Ser Gly Glu Glu Lys Phe Pro Gly Val Val Arg Phe Arg Gly Pro	
336 140 145 150	
338 ctg tta gca gag agg aca gtc tcc gga ata ttc ttt gga gtt gaa ttg	892
339 Leu Leu Ala Glu Arg Thr Val Ser Gly Ile Phe Phe Gly Val Glu Leu	
340 155 160 165	
342 ctg gaa gaa ggt cgt ggt caa ggt ttc act gac ggg gtg tac caa ggg	940
343 Leu Glu Glu Gly Arg Gly Gln Gly Phe Thr Asp Gly Val Tyr Gln Gly	
344 170 175 180	
346 aaa cag ctt ttt cag tgt gat gaa gat tgt ggc gtg ttt gtt gca ttg	988
347 Lys Gln Leu Phe Gln Cys Asp Glu Asp Cys Gly Val Phe Val Ala Leu	
348 185 190 195	
350 gac aag cta gaa ctc ata gaa gat gat gac act gca ttg gaa agt gat	1036
351 Asp Lys Leu Glu Leu Ile Glu Asp Asp Asp Thr Ala Leu Glu Ser Asp	
352 200 205 210 215	
354 tac gca ggt cct ggg gac aca atg cag gtc gaa ctt cct cct ttg gaa	1084
355 Tyr Ala Gly Pro Gly Asp Thr Met Gln Val Glu Leu Pro Pro Leu Glu	
356 220 225 230	
358 ata aac tcc aga gtt tct ttg aag gtt gga gaa aca ata gaa tct gga	1132
359 Ile Asn Ser Arg Val Ser Leu Lys Val Gly Glu Thr Ile Glu Ser Gly	
360 235 240 245	
362 aca gtt ata ttc tgt gat gtt ttg cca gga aaa gaa agc tta gga tat	1180
363 Thr Val Ile Phe Cys Asp Val Leu Pro Gly Lys Glu Ser Leu Gly Tyr	
364 250 255 260	
366 ttt gtt ggt gtg gac atg gat aac cct att ggc aac tgg gat gga aga	1228
367 Phe Val Gly Val Asp Met Asp Asn Pro Ile Gly Asn Trp Asp Gly Arg	
368 265 270 275	
370 ttt gat gga gtg cag ctt tgt agt ttt gcg tgt gtt gaa agt aca att	1276
371 Phe Asp Gly Val Gln Leu Cys Ser Phe Ala Cys Val Glu Ser Thr Ile	
372 280 285 290 295	
374 cta ttg cac atc aat gat atc atc cca gct tta tca gag agt gtg acg	1324
375 Leu Leu His Ile Asn Asp Ile Ile Pro Ala Leu Ser Glu Ser Val Thr	
376 300 305 310	
378 cag gaa agg agg cct ccc aaa ctt gcc ttt atg tca aga ggt gtt ggg	1372

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number